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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Wu.K., Tian,L., Malik,K., Brown,D. and Miki,B.
Direct Submission
Submitted (ube: 0.007-1999) Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-Food Canada, Ottawa, Ontario KIA 0C6, Canada
Location/Qualifiers
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                                                                             ggtcacataagagatgttggcgctgaaaagggaaatactatgctctaaatgttccacta
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                             541 GCTGATATCGCTATCAATTGGGGCGGTGGGCTTCACCATGCTAAGAAAAGCGAGGCTTCT
                                                                 gggtttttgctatgtaaacgacatcgtgctaggggattctggagttgctcaagatgtttaag
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/LTAIN 1 1 1 101 - MKWWOENLYULEVKERLAKDCTSLPLGKYGRDDEDMILWFL
KPRRESYDEALGKLTKA I VSSSLCFLVILLS I LAVNESKKLEPETSLLCHTCR IK SHVVP
CFGNIDKVDELSEDSIKAATDTGKRYVHGFLDVKGRPVVI VAPAKHI FGILLDP I EDEK
LCVFILLERALSKLENGRAGGHKI LIGI FDLAGFGSONADLKFLTFLEFDVYYYY PSRIJDEVI,
FVDAPE I FQP I WQFTKPLVKQYASLVKFCSAETVRKEYFTEETLPSNFRS*
                       VVGPLIIALYIKMFQGLCSLYAFCFNQTIKMIRNLPSYYLVAYQYIADGKLKDDVKAL
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SVVGVHNGKKFNEIVIKPEMIGHYLAEFSMTCKKVNHHRPRICGCCCFRRSTRFIPLR
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DEPGEB ILVEBGWHHOVYNLEDTISINHWLARYNLGWWWDLLWKDYKUTEESIEDIR
DICDDFEAICQRNLAANTGMWNLDFPLEMSRFSLGNWVLLGSYSDKHYNLNSCSLANA
ONLLMNLSTILKVWMKHISAGGVTAEEVYLDIRETLEDDOFLRRYRDMGFTYARIHME
COMPLEMENT (17358. 17918)
//octe-*gb|AAB60312.1
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REDWYSENGNPNLHVFATHFGKSRVQVADCDTREFTDGKRLEMSYTEFVEGWTNKDSI
EESVLYLKDWHFVKEYPDYTAYQTPPILFSDDWLNVYLDNYQMHEDRDSFQKYDGISCS
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KIFGASNVTKLLNELLPHOREDAVNSLAYEAFARVRDPVYGCVGAISYLQRQVHRLQK
ELDAANADLAHYGLSTSAAGAPGNVVDLVFQPQPLPSQQLPPINPVYRLSGASPVMNQ
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IKELQDPQVWEDLKSRLRYRGRIMVNVGGKCVEAEDSDRDGALVWEETLRVWSQVFGD
KRFVTIGNGNDSSYALTGDLPDLDAWKKRLPRSELRSYVDWNIPYRREFCLRY
COMPLEMENT (join(24469. .24538,24651. .24781,24879. .24969,
25228. .23370,25465. .25905,26323. .26862))
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                                                     VFKPVVAIKNTDYKELTRTKLKOPOEWIIEKYLDFVESVWPYYCRTIRFLKRANLJ!"
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4376. 4501,4560. 4886))
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GNIHSISFLLKTLTDSYFDVFATLPPIIPPGPIGILGFGAGSTARLILELYPPEIAVH
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9663. .9743,9997. .10118,10216. .10378,10488. .10625,
10747. .10956.)
//note="qene_id:WDC12.4
unknown protein"
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/product=+40s ribosomal protein S15-like protein"
/protein_id==man10549.1
/db_xref="G1:10177288"
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similar to unknown protein"
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complement(23069, .24058)
/note="gene_id:MDC12.6
unknown protein"
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/db_xref="GI:10177287"
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/db_xref="G1:10177289"
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/note="gene_ld:MDC12.3"
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Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SpliceFredictor (Volker Brendel) Stanford University, http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi).

Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE (Sean Eddy, Mashington University School of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5 clone is MH122 and the 3 clone is K9H21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (sites)
Nakamura,Y., Sato,S., Kaneko,T., Kotani,H., Asamizu,E., Miyajima,N.
and Tabata,S.
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FTEIRKAESLOSTKNTVWSNFWSLDAAIKIPLLFVPAFLAVYAICGAEVTKELSPWW
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                 1621 TGAIGTITITICAGCAACCTTTTGAGTICTGTGAAAACGCTGCATTGATTAGAACAGTGA 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui P1
                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MDC12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Structural analysis of Arabidopsis thaliana chromosome 5. III. Sequence features of the regions of 1,191,918 bp covered by seventeen physically assigned Pl clones DNA Res. 4 (6), 401-414 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (24-OCT-1997) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
Te:81-438-52-3935, Fax:81-438-52-3934)
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/organism="Arabidopsis thallana"
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join(2581. .2816,3020. .3434)
/note="gene_id:MDC12.1
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/chromosome="5"
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NIFGFDVKDALKSINAAFAPALASKIPWVATLGNHDQESTFTRQQVNNHTVKLPNTLS
OVNPPEAANTUDGFCNNVLQHGAADSKLQNKSVLNLVFLDSGDYSSVYNWEYPWEGYDWIK
TSQQFWFDRTSKRLKERVNKPNPQGSTAPGLAYFHTPLPFFLSFDSKNATKGVRQDS
TSAASTNSGFFTTLIARGDVKSVFVGHDHVNDFCGELKGLNLCYGGGFGYHAYGKRGM
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SVDRSISFSELMKKLYEFCGYSVDLRCQLPNGDLETLISVKSEEELAEIVEEYDRICG
AKIRAVLSPPRSSHKTESSPSSSGDRSPKSPFSVTPSPPNSPSPAYGRYLQSRYCLPS
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                                                                                                                                                                                            SLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGGGYTTRNYARCMCYETA<sup>V</sup>AVGV
EPDNKLPYNEYFEY FGPDYTLHVDPSPMENLNTPKDMERTRNTLLEQLSGLTHAPSVQ
FQHTPPVNRVLDEPEDDMETRPKPRTWSGTATYESDSDDDDKPLHGYSCRGGATTDRD
                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSYGRGGERGGYGO GEDRUGGGRGGGGRGGSSKRELDSVSLPKONFGNLYHFERDSY
YVESPTYQAMTEQDVAMYRTERDISVEGRDVPKPMKMFQDDANPPDNLLEALAKGFTK
PTPIQAQGWPWALKGRDLIGIAETGSGKTLAYLLPALVHVSAQPRLGQDDGPIVLILA
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EGOFFULKRYTYLVLDEADRALLDNGFBEQIRK TYSQIRPDROYLLLWSATWPREVETLA
ROFERDPYRAIIGTSTRAWQSINOVIEIVPPEKYNRLLTLKQLMGSKILIFVET
KRGCDQVTRQLRRDGWPALAIHGDKTQSERDRVLAEFKSGRSPIMTATIVAARGLUVR
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VPPTLSALVRSSGSSYGGSGGRRFRPRGGRGGGFGDKRSRSTSNFVPHGGKRTW"
join (31825. .31984, 32074. .32492)
//note="gene_idimCol2.9"
unknown_protein"
                                                                                                                      LRRFNVGEDCPVFDGLFDFCRASAGGSIGAAVKLNRQDADIAINWGGGLHHAKKSEAS
GFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGVEEAFYTTDRVWTVSFHKFGDFFP
                                                                                                                                                                                                                                                                           complement(join(27602. 27720,27816. 28049,28572. 28798, 28899. 28984,29089. 29181,29350. 29504,29589. 29750, 29842. 30021,30108. 30546))
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/codon_start=1
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                                                                  /translation-"MEADESGISLPSGPDGRKRRVSYFYEPTIGDYYYGQGHPMKPHR
                                                                                               IRMAHSLIIHYHLHRRLEISRPSLADASDIGRFHSPEYVDFLASVSPESMGDPSAARN
                                                                                                                                                                    GTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRPLIQKVMEVYQPEAVVLQCGAD
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join(36872. .37172,37302. .37699,37781. .38251)
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deacetylase"
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/product="tRNA-Thr(TGT)"
38879. .39295
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  gagtatgttgacttcctcgcttccgtttcgccggaatctatgggcgatccttccgctgca
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Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
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Pipal,A. and Wegener,S.
Pirect Submission
Submitted (28 47N-1998) Microbiology-Medical School, University of Innsbruck, Filtz-Preql-Strasse 3, Innsbruck A-6020, Austria
Location/Qualifiers
                                                                                                                                                                      25542 TCTTACAACGITCCTCTCATGGTGTTGGGTGGAGGGTATACTATTCGAAATGTTGCC 25483
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cggttgggttgcttcaacttatcagtcaaqggtcacgctgattgccttcggttcttaaga
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Zea mays histone deacetylase (hdlb) mRNA, complete cds.
AF045473
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/product="histone deacetylase"
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/db_xref="G1;4193320"
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PHRIRMAHSLVVHYGLHRLLELSRPYPASEADIRRFHSDDYVAFLASATGNPGVLDPR
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                                                                                                                                                                                               Score 615.6; DB 8;
Pred. No. 9.1e-163;
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/protein_id-"AAD10139.1"
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                                                                                                                                                  453
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1378. .1742
/gene="hdlb"
                                                                                                                                                                                              34.28;
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Matches 853; Conservative
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ORIGIN
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us-09-645-337-3.rge

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/product "histone deacetylase HDA101"
/protein_id="AAK67142.1"
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KPHRIMTHSLLARGLNOMOVYRNPARRDLCRFHADDYINFLRSYTPFTOODOJ
RLLKRFNVGEDCPVFDGLYSFCQTYAGASVGGAVKLNHGHDIAINWSGGLHHAKKCEA
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUN-2001
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1 (bases 1 to 1906)
Chandler, V.L., Kaeppler, S.M., Kaeppler, H.F. and Cone, K.C. Sequences from the Plant Chromatin Consortium (NSF Plant Genome project 9975930)
                                                                                                                                                                                                                                                   ttcggcccagattatacgcttcatgtcgacccaagtcctatggagaatttaaacacgcc 1224
                                                                                                                                                                                                                                                                                                                                                                                   gcagttgctgttggagtagagccggacaacaacaccttacaatgagtattttgagtat 1164
                                                                                                                                                                                                                                                                                                                                             1048 TTTGGCCCTGATTATACTCTTCATATCCAACCAAAAAGTGTTGAAAAGCCTGAATACCACA 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                               cctagogiccagitticagcacaccaccagicaategagittiggacgageeggaagai 1344
                                                                         985 tcagtcaagggtcacgctgattgccttcggttcttaagatcttacaacgttcctctcatg 1044
                                                                                                                                                   1045 gtgttgggtggtgaagggtatactattcgaaatgttgcccgttgctggtgttatgagact 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1168 CCCAGCACTCAATTCCATGACAGACCGTCAGACCCTGAAGCTCCAGAGGAGAAGAGGGAG 1227
                                                                                             Zea mays histone deacetylase HDA101 (hda101) mRNA, complete AF384032
925 gttgttetteagtgtggtgetgaeteettaagtggtgateggttgggttgetteaaetta
                                   GITGICCICCAATGCGGAGCTGACTCTTTGGCTGGAGACAGGTTAGGTTGCTTCAACCTG
                                                                                                                                                                           Bergstrom,D., Springer,N.M., Schmitt,L.T., Guthrie,E.,
Sidorenko,L., Selinger,D., Kaeppler,S.M. and Cone,K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="hda101"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-MAY-2001) Biological Sc
Tucker Hall, Columbia, MO 65203, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1345 gacatggagacaagaccaaaacctcgca 1372
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/cultivar="B73"
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38. .1591
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PGTGD1RD1GHSKGKYYSLNVPLDDG1DDESYQSLFKPIMGKVMEVFRPGAVVLQCGA
DSLSGDRLGCFNLS1KGHAECVRYMESFNVPLLLLGGGGTJTRNVAKOWCYETGVALG
DSPEDKMPVNEYYETFVEDPYTLHVAPSNMENKYNTRQQLDD1RSKLLDNLSKLRHAPSY
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NATRVQDGGRVASEHRGLEPMAEDIGSSKQAPQADASAMAIDEPSNVKNEPESSTKLQ
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SGFCYVNDIVLAILELLKHHERVLYVDIDIHHGDGVEEAFYTTDRVMTVSFHKFGDYF
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                                                                                                                                                                                                                                                                                                       183 cagttacttctacgagccgacgatcggagactactactacggtcaaggccacccgatgaa
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                                                                                                                                                                                                                                                                                                                                                                                                    172 GCCGCACCGCATCCGGATGACGCACTCGCTGCTGCCGCCTACGGCCTCCTCAACCAGAT
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                                                                                                                                                                            Score 549.6; DB 8;
Pred. No. 4.2e-144;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 2047)
Rossi, V., Hartings, H. and Motto, M. Identification and characterisation of an RPD3 homologue from maize Sea mays L.) that is able to complement an rpd3 null mutant of Sacharomyces cerevisiae
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QEPEDKMPVNEYYEYEGPDYTLHVAPSNMENKNTRQQLDDTRSKLSKLRHAPSVHFQE
RVPDTETPEQDEDQDDPDERHDPDSDMEVDDHKAVEESSRRSTLGTKTKREFGENATR
VQDGGRVASEHRGLEPMAEDIGSSKQAPQADASAMAIDEPSNVKNEPESSTKLQGQAA
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/translation="MDPSSAGSGGNSLPSVGPDGQKRRVCYFYDPDVGNYYYGQGHPM
KPHRIRMTHSLLARYGLLARYGLLANGMOYYRPPREFERENCEFFIAEET NFLEXTYPETQDD01
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PGTGDIRDIGHSKGKYYSLNVPLDDGIDDESYQSLFKPIMGKVMEVFRPGAVVLQCGA
                                                                                                                                           1143 ttacaatgaytattttgagtatttcggcccagattatacgcttcatgtcgacccaagtcc 1202
                                              1023 atcttacaacgttcctctcatggtgttgggtggtgaagggtatactattcgaaatgttgc 1082
                                                                         943 GTCTTCAACGTCCATTGTTGCTCCTTGTGGTGGTGGTATACCATAAGAAATGTTGC 1002
                                                                                                                                                                                                                                                                                   1063 IGTTAATGAGTACTATGAATACTTCGGTCCAGATTACACTCTTCATGTTGCACCAAGTAA 1122
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883 TAGGTTGGGCTGCTTCAACCTCTCAATCAAAGGTCATGCGGAATGTGTTAGGTATATGAG
                                                                                                                                                                                                                                                                                                                                 1203 tatggagaatttaaacacgcccaaagatatggagaggataaggaacacgttgctggaaca
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Rossi,V., Hartings,H. and Motto,M.
Direct Submission
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/strain="W22"
/db_xref="taxon:4577"
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                                                                                                       Length 2047;
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                                                                                                     Score 525.2; DB 8;
Pred. No. 3.4e-137;
0; Mismatches 388;
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66.68;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; euroslas II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases i to 1807)
Wu,K., Mikl,B.L., Tian,L. and Brown,D.C.
Wepressing gene expression in plants
Patent: EP 1094112-A 1 25-PRP-2001;
The Minister of Agriculture and Agri-Food (CA)
Location/Qualifiers
                              1083 ccgttgctggtgttatgagactgcagttgctgttggagtagagccggacaacaactccc 1142
                                                                                                1143 ttacaatgagtattttgagtatttcggcccagattatacgcttcatgtcgacccaagtcc 1202
                                                                                                                   tatggagaatttaaacacgcccaaagatatggagagataaggaacacgttgctggaaca 1262
GTCTTTCAACGTTCCATTGTTGCTCCTTGGTGGTGGTGGATATACCATAAGAAATGTTGC 1105
                                                                                                                                                                                                                                     actiticgggactaatacacgcacctagcgtccagtitcagcacaccaccagtcaatcg 1322
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Pred. No. 1.1e-136;
0; Mismatches 396;
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/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                         506 CIGGAGGATCIGITGGTGGCTCTGTCAAGCTTAACCACGCCTCTGCGATATTGCCATCA
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PPDTFTPEVDEDOGDGTKWNPPSDMDYDDDRKPIFSTRYRRANGGRAFYBYFGT
386 C
464 9 485 L
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                                                                                        2 (bases 1 to 1807)
Wu,K., Tlan,L., Malik,K., Brown,D. and Miki,B.
Direct Submission
Submitted (lasocr-1999) Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-Food Canada, Ottawa, Ontario KIA 0C6, Canada
Location/Qualifiers
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Wu,K., Malik,K., Tian,L., Brown,D. and Miki,B.
Functional analysis of RPD3 histone deacetylase homologs in
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/protein_id-"AAG28474.1"
/db_xref-"GI:11066139"
                                                                                                                                                                                                               /organism-"Arabidopsis thaliana"
/cultivar-"Columbia"
/cultivar-"Columbia"
/clone-"Glic3"
1. 1807
/gene-"RPD3A"
/gene-"RPD3A"
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Arabidopsis thaliana Rakaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II: Brassicales; Brassicaceae; Arabidopsis. 2 (bases 1 to 1808)
Tomihama,T., Shoji,K., Hanyu,H. and Okano,T.
Direct Submission
Submitted (16-JUL-1997) Department of Biology, Central Research
Institute of Electric Power Industry, 1646, Abiko, Chiba 270-11, 12-AUG-1997 complete cds. ü 1 (bases 1 to 1808)
Fomihama,T., Shoji,K., Hanyu,H. and Okano,T.
Characterization of a histone deacetylase (EST G11G3T7) AF014824 1808 bp mRNA PLN Arabidopsis thaliana histone deacetylase mRNA, AF014824.1 GI:2318130 Arabidopsis thaliana thale cress Unpublished AF014824 DEFINITION ORGANISM AUTHORS TITLE TITLE JOURNAL ACCESSION VERSION KEYWORDS REFERENCE JOURNAL REFERENCE AUTHORS AF014824 SOURCE LOCUS

RESULT

Location/Qualifiers

Japan

FEATURES

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1QDIGYGSGKYYSLNVPLDDGIDDESYHLLEKPIMGKVMEIFRPGAVVLQCGADSLSG
DRLGCFULSIKGHAECVKFMRSFNVPLLLLGGGGYTIRNVARCWCYETGVALGVEVED
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ERGKCCEVEVDESQETKYTGVNPOVYEEASVKMEEEGTNKGGAEQAFPRT*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 GCGCCAATTCGCTGGCGTCCGGACCTGATGGTGAAGAGGAAAGTTTGTTATTTCTATG 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 ACCCTGAGGTCGGCAATTACTACTATGGCCAAGGTCATCCCATGAAGCCCATGACGATCC
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                                                                                                                                                                                                                                                                                                                                                                      Score 523.4; DB 8;
Pred. No. 1.1e-136;
                                                                                                                                                                                                                                                                                                                                                                                                      396;
             /organism~"Arabidopsis thaliana"
/strain="Columbia"
                                                           /note="EST clone No.GllC3T7"
                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                             /db_xref-"taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                        29.1%;
65.9%;
                                                                             .1648
                                                                                                                                                                                                                                                                                                                                                                                                      777; Conservative
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ALKRFNVGEDCPVFDGLYSFCQTYAGGSVGGAVKLNHGHDIAINWAGGLHHAKKCEAS
GRCYWNIYVALILELLKYHOVLYVDIJHHGROVEBARFYTDRVMYVSFHKFDDYFP
GTGDIRDIGYSEGRYYKCLNVPLDDGIDDDSTRFPIISKWAEWARPGAVLQCGAD
SLSGDRIGGFNLSGKGHAECVKFWRSFNVPLLLLGGGGGYAIRNVARCWCYETGVALGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation-"MDASAGGGGNSLPTAGADGAKRRVCHFYDAEVGNYYCGQGHPMKPHRITAHTHALLAHYGLLDQMQVLKPHPARDRDLCRFHADDYVAFLRSVTPETQQDQIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 1579)
Song,F. and Goodman,R.M.
Molecular characterization of a rice histone deacetylase gene OsHD1
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Suogy F. and Goodman, R.M.
Direct Submission
Submitted (30-DEC-2000) Department of Plant Pathology, University
of Wisconsin-Madison, 1630 Linden Drive, Madison, WI 5706, USA
Location/Qualifiers
1. 1579
                                                                                                                                                                                                                                                    987 TCAATCTTTCAATCAAAGGTCATGCTGAGTGCGTCAAATTTATGAGATCGTTCAATGTTC 1046
                                                                                                                                                                                                                                                                                              eteteatggtgttgggtggaagggtataetattcgaaatgttgeeegttgetggtgtt 1096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1227 ATTCTCGTCAGATGCTTGAAGAGATTCGCAATGACCTTCTCCCACAATCTCTTAAGCTTC 1286
                                                                                                                           916
07-FEB-2001
                                         atgaaagtttccgcagcttgtttagacctcttatccagaaggttatggaagtgtatcagc
                                                                                                                         tcaacttatcaqtcaagggtcacgctgattgccttcggttcttaaggatcttacaacgttc
                                                                                                                                                                                                                                                                                                                                                                                 atgagactgcagttgctgttggagtagagccggacaacaactcccttacaatgagtatt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1167 ATGAATACTTTGGTCCAGACTATACACTTCACGTTGCTCCAAGTAACATGGAAATAAGA
                                                                                 ATGAGAGCTATCATCTGTTATTCAAGCCCATCATGGGGAAAGTTATGGAAATTTTCCGAC
                                                                                                                                                                                                                                                                                                                                       1047 CCCTACTGCTCTTGGGTGGTGGTGGTTACACTATCCGCAATGTTGCCGGTTGCTGGTGCT
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/db_xref="G1:12698880"
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/db_xref="taxon:4530"
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13. .1494
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AF332875
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ELTDKMPPNEYFEYFGPEYSLFVAASNMENRNTNKQLEEIKCNILDNLSKLOHAPSVO
FEER (PETKLPEPDEDQEDPDERHDPDSDMVLDDHKPMGHSARSLIRNIEVKREITES
EAKOOHGKRLTTEHKGPEPMADDDPGSSKQAFVSRRLLYPSANP"
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                                                                                                                                                                                                                                        CCGACGCGGGGGCCGACGGGCCGAGCGGCGGGTGTGCCACTTCTACGACGCGGAGGGG 108
                                                                                                                                                                                                                                                                                                              agectaateatteactateaceteeacegtegettagaaateagtegeeetageeteget 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tegeceggaatetatgggegateetteegetgeaegaaaeetaaggegatteaatgteggt 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gaggattgtcctgtcttcgacggactttttgattttgccgtgcttccgccggaggttct
                                                                                                                                                                                                                                                                                                                                                                                                       169 GCGCTGCTCGCCCACTACGGCCTCCTCGACCAGATGCAGGTGCTCAAGCCCCACCCGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggagactactactacggtcaaggccacccgatgaagcctcaccggatccgtatggctcat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            289 ACGCCGGAGACCCAGCAGGACCAGATC-----CGGGCGCTCAAGCGCTTCAACGTCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        748 ttccacaaatttggggactttttcccaggaactggtcacataagagatgttggcgctgaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             640 TICCACAAGTIIGGGGAITATITCCCGGGAACAGGGGAIAICCGIGACATIGGGIATICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     808 aaagggaaatactatgctctaaatgttccactaaacgatggtatggacgatgaagtttc
                                                                                                                                                                               6
                                                                                                                                           Length 1579;
                                                                                                                                                                               Indels
                                                                                                                                     Score 503.8; DB 8;
Pred. No. 3.6e-131;
0; Mismatches 417;
                                                            420 g
                                                                                                                                     28.0%;
64.8%;
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                                                                                                                                                                       Matches 783; Conservative
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ORIGIN
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NVGEDCPVFDGLTSFCQTYAGGSVGGAVKLNHGLCDIAINWAGGLHHAKKSEASGFCY
VNDIVLAILELLKVHERVLYVDIDIHHGDGVEEAFYTTERVMTVSFHKFGDYFPGTET
FVYIGYGKGKYYSLNVPLDDGIDDESYQSLFKPIMGKVWEIFKPGAVVLQCGADSLSG
DRLGCFNLSIKGHAECVKYMISFNVPLLLVGGGGTTIRYVARCWCYFTGVALGFELDD
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MTHALLAHYGLLQHMQVLKPVPARDRDLCRFHADDYVSFLRGITPEMQGDQLRQLKRF
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PPEAEIPEEDEDQHDPEGRWDPDSDMEVDDRSISIRSRVKREIMEPDLKDRDDVKDAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophylidae; Caryophyliales; Alzoaceae; Mesembryanthemum. 1 (bases 1 to 1839) Scharte, J. and Baur, B.
                                                                                                                                                                           1287
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                                                   1108 gttgctgttggagtagagccggacaacaactcccttacaatgagtattttgagtatttc 1167
                                                                                                                                                                                                                                                                                                                                             1288 agcgtccagtttcagcacaccaccagtcaatcgagttttggacgagccggaagatgac 1347
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940 CTTGGTGGTGGTGGATATGCCATAAGAAATGTTGCACGCTGTTGGTGCTATGAGACAGGA 999
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Submitted (27-JUN-2000) Institut fuer Botanik, Universitaet
Muenster, Schlossgarten 3, Muenster 48143, Germany
                                                                          1000 GTTGCACTTGGTCATGAGCTCACGACAAGATGCCTCCAAATGAGTATTTTGAGTATTTTG
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/db_xref-"taxon:3544"
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/gene** Hdeac1*
/codon_start*1
/product-*histone_deacetylase*
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/db_xref-"G1:9022439"
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Scharte, J. and Baur, B.
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                  Indels
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0; Mismatches 448;
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Best Local Similarity
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LYRKADIRPHKATADEMTKFWCDEYVRFLRSIRPDNNSETNKOMQRFWGEOCPVFDG
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LKYPCOVETY DIDVHGDGVEREAFYTTDRVWTVSFHRYGEYPGTGDLRDIGAGKGKY
YANNIPLRDGMDDDAYESIFVPISKVWETFQPAAVULQCGADSLTGDRLGCFNLTVK
GHCKOYEFVKKYNLPFLMVGGGGYTIRKVSRCWTYETSVALAFIANELDFNDISDD
EDKVONDRLEDGSDROKRIVPENEYSDSEDGEGGRRONRSYKGGRRRPRLDKSDTNSK
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1183 CTCAACATGAATACTATGAGTATTTCGGTCCTGACTATACTCTCCACGTTGCTCCGAGTA 1242
                                                                                                                                                                                1303 ACCTCTCAAGTCTACAGCATGCACCAAGTGTGCAATTCCAAGAACGTCCACCTGAAGCTG 1362
                                                              The histone deacetylase RPD3 counteracts genomic silencing in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JAN-1997
                                                                                                                     1243 ATATGGAGAACAAGAACTCCCGACCAATGCTGGATGATATAGAGGAAAGCTTCTTGAGT
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 2172)
De Rubertis, P., Kadosh, D., Henchoz, S., Pauli, D., Reuter, G.
Struhl, K. and Spierer, P.
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/clone_lib="cDNA library (Brown and Kafatos)"
/map="648C"
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D.melanogaster mRNA for putative histone deacetylase.
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/db_xref="FLYBASE:FBqn0015805[FBa10045042]"
/db_xref="SWISS-PROT:Q94517"
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/db_xref="taxon:7227"
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/product="histone deacetylase"
/protein_id="CAA70455.1"
/db_xref="G1:1666637"
                                                                                                                                                                                                                                                                                                      gagttttggacgagccggaagatgacatggagaca 1356
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Nature 384 (6609), 589-591 (1996)
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histone deacetylase; RPD3 gene
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/gene="RPD3"
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                                             gtaagcggcgagtcagttacttctacgagccgacgatcggagactactactacggtcaag 229
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                                                                                                                                                        414 TCCACTGCGACGAGTACGTCCGGTTCTTGCGATCCATTCGGCCGGACAACATGTCGGAGT
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                           6
  Length 2172;
                        Indels
                       0; Mismatches 395;
  Score 462; DB 3; |
Pred. No. 2.5e-119;
  Score 462;
25.7%;
64.3%;
                       Conservative
           Similarity
                    Matches 728;
 Query Match
             Best Local
                                                                   237
                                             170
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/traislation-"MAYSOGGCKKKVCYYYDGDIGNYYGGGHPMKPHRIRMTHNLLL
NYGLYRKMEIYRPHKATAEEMTKYHSDEYIKFLRSIRPDNMSEYSKOMORFNVCEDCP
VFDGLFEFCQLSTGGSVAGAVKLNROOTDMAVNWAGGLHHAKKSEASGFCYVNDIVLA
ILELLKYHORVLYIDIDIHHGDGVEEAFYTTPRVMTYSEVSWYNNFPGTGDLKDIGAG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus;
1 (bases 1 to 1878)
1188 CCAACGAACTGCCCTACAACGATTACTTCGAGTACTTTGGGCCCGGATTTTAAGCTGCACA 1247
                                                                   1248 TTAGTCCCAGCAATATGACAAATCAGAATACATCCGAGTACCTGGAGAAGATCAAGAACC 1307
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Submitted (23-DEC-1997) Blochemistry, Miyazaki Medical Collage,
Kiyotake Kihara 5200, Miyazaki 889-16, Japan
Location/Qualifiers
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Chicken histone deacetylase-2 controls the amount of the IgM
H-chain at the steps of both transcription of its gene and
alternative processing of its pre-mRNA in the DT40 cell line
J Biol. Chem. 274 (34), 23977-23990 (1999)
                               1190 tegacecaagteetatggaaatttaaacaegeecaaagatatggagaggataaggaaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 agccgacgatcggagactactactacggtcaaggccacccgatgaagcctcaccggatcc
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                                                                                                  Gallus gallus histone deacetylase-2 mRNA, complete cds.
AF039752
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/protein_id="AAB96924.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 459.2; DB 5;
Pred. No. 1.5e-118;
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/organism="Gallus gallus"
/db_xref="taxon:9031"
71. .1537
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Takami, Y.
                                                                                                                                                                                                                              1878 bp
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                                                   240 CCCACAAAGCTACTGCTGAGGAAATGACCAAGTACCATAGTGATGAATACATCAAATTTC 299
                                                                               436
                                                                                                       300 TCAGATCAATAAGGCCTGACAATATGTCTGAGTACAGC-----AAGCAGATGCAAAGAT 353
                                                                                                                                                             354 TTAATGTTGGAGAAGATTGTCCTGTATTTGATGGCCTGTTTGAGTTTTTGTCAGCTGTCAA 413
180 GAATGACTCACAACTTGCTCCTAAATTATGGCTTGTACAGGAAAATGGAAATTTACCGAC 239
                        ctageetegetgaegeeteegatateggeegatteeettegeeggagtatgttgaettee
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                                                                               tegetteegtttegeeggaatetatgggegateetteegetgeacgaaacetaaggegat
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Lyrkmbiyrphkatadbemykfhsdbyvrflrsirpdnmseynkomorfnvgencpvfd
Glydfcqlsaggsvaaavklnkqaseicinmggglhhakkseasgfcyvndivlgile
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YAVNIPLENGONDDDAYEISTPVIISKWETFPGAAVULGGABSLLGGENLGY
KGHGKCVEFVKKYIDFLMYVGGGGYTIRKGRCWTYETSVALAVEIANELPYNDYFE
YFGPDFKLHISPSNMTNONTSEYLEKIKNRLFENLRMVPHAPGVQIQAIPEDAINDES
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SNKASSETSSEIKDEKEKGDGADGEESTASNTNSNNKSDNNKSDNDAGATANAGSGSGT
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Johnson, C.A., White, D., O'Neill, L.P. and Turner, B.M.
Direct Submission
Submitted (26-SEP-1997) Anatomy, Univ. of Birmingham, Birmingham
B15 2TT, U.K.
                                                                                                                                                           AF026949 2073 bp mRNA INV 22-JUN-1998
Drosophila melanogaster putative histone deacetylase HDAC1 mRNA,
                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
Bukaryota; Metazoa; Arthopoda; Tracheata; Hexapoda; Insecta;
Pteryota; Metazoa; Arthopoda; Tracheata; Brachycera;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (Dassas 1 to 2073)
Johnson, C.A., White, D., O'Neill, L.P. and Turner, B.M.
Putative histone deacetylase HDACI from Drosophila melanogaster
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/db_xref="taxon:7227"
/chromosome="3"
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577 CGGAAGCCTCCGGCTTCTGCTACGTCAATGACATTGTTCTGGGAATTCTGGAACTGCTTA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammallai; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1985)
                       12-JAN-2001
                       PAT
                   DNA
WO0071703.
                AX053103 1985 bp
Sequence 27 from Patent AX053103
                                                                  AX053103.1 GI:12227158
                                                                                                                      Homo sapiens
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                                DEFINITION
                                                  ACCESSION
VERSION
                                                                                                                   ORGANISM
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AX053103
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SOURCE

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963 teggitigggitigetteaactiateagteaagggiteaegetgaligeetleggilettaag 1022
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                                                                                                                                                           Length 1985;
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                                                                                                                                                          Score 444.6; DB 6;
Pred. No. 2.1e-114;
0; Mismatches 454;
Macleod, A.R., Li, Z. and Besterman, J.M.
Inhibition of histone deacetylase
Patent: WO 007103-A 27 30-NOV-2000;
Methylgene, Inc. (CA)
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                                                                           /organism="Homo sapiens"
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                                                   Location/Qualiflers
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Best Local Similarity 61.4%;
Matches 733; Conservative (
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Search completed: March 9, 2002, 00:54:32 Job time: 4519 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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 nucleic search, using sw model OM nucleic March 8, 2002, 23:17:23; Search time 125.93 Seconds Run on:

(without alignments) 12254.311 Million cell updates/sec

US-09-645-337-3

1 gtgcccacaactcctagtaa.....acgcgtgcatgcgacgtcat 1800 Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

930621 seqs, 428662619 residues Searched:

1861242 hits satisfying chosen parameters: Total number of

seq length: 0 seq length: 2000000000 Minimum DB : Maximum DB : Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
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m	1606.4			21	AAC46043	Arabidopsis thali
7	614			20	AAX90837	Maize histone dea
S	549.6				AAX90840	Maize histone dea
9	530.2				AAX90839	Maize histone dea
7	523.4			22	AAF80350	Nucleotide sequen
5 0	518.8				AAZ58259	Rice histone deac
6	497.2					Soybean histone d
10	444.6					Human METH2 relat
11	444.6					And Alala

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WPI; 2001-258457/27. P-PSDB; AAB67812.

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ALIGNMENTS

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Histone deacetylase; AtRPD3B; RPD3; gene expression; transgenic plant; HDA1; ethylene-responsive phenotype; hypocotyl elongation; ds.
                                                                        Nucleotide sequence of a histone deacetylase designated AtRPD3B.
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                                                      (first entry)
                                                                                                                      Arabidopsis thaliana.
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                                                    29-JUN-2001
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        AAF80351
RESULT
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Methods for regulating gene expression in transgenic plants, e.g. repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotylelongation), comprises introducing genes encoding histone deacetylase

91pp; English 18; 9; F1g Claim The present sequence encodes an Arabidopsis thaliana histone deacetylase designated AtRPD3B. The protein is homologous to yeast RPD3 and HDA1. The polynucleotide sequence is used in the method of the invention. The specification describes a method for regulating gene expression in transgenic plants. The method comprises modifying histones by introducing chimeric nucleotide sequences which have regulatory elements in operative association with a gene of interest or with a nucleotide sequence encoding histone deacetylase. The method is useful for regulating the particularly for repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation). The method is also useful as a functional test for identifying a phenotype associated with perturbing a gene. The histone deacetylase genes are useful for altering the development of an organism.

Sequence 1800 BP; 478 A; 390 C; 456 G; 476 T; 0 other;

ö 120 240 300 300 360 360 420 420 480 540 540 Gaps 9 9 gtgcccacaactcctagtaatgactttctcaggcattgttgacacaaattttgctctgag algaggcagacgaaagcggcalclclctgccglcgggacccgacggacgtaagcggcga gtcagttacttctacgagccgacgatcggagactactactaccggtcaaggccaccgatg gtgcccacaactcctagtaatgactttctcaggcattgttgacacaaattttgctctgag gtcagttacttctacgagccgacgatcggaggctactactacggtcaaggccacccgatg aagcctcaccggatccgtatggctcatagcctaatcattcactatcacctccaccgtcgc ttagaaatcagtcgccctagcctcgctgacgcctccgatatcggccgattccattcgccg ttagaaatcagtcgcctagcctcgctgacgcctccgatatcggccgattccattcgccg gagtatgttgacttcctcgcttccgtttcgccggaatctatgggcgatccttccgctgca cgaaacctaaggcgattcaatgtcggtgaggattgtcctgtcttcgacggactttttgat gctgatatcgctatcaattggggggggggttggcttcaccatgctaagaaaagcgaggcttct gctgatatcgctatcaattggggggggggttgggcttcaccatgctaagaaaagcgaggcttct 999ttttgctatgtaaacgacatcgtgctagggattctggaggttgctcaagatgtttaag ö Length 1800; Indels 1; 22; DB 0; Mismatches 99.9%; Score 1799; 99.9%; Pred. No. 0; Conservative Best Local Similarity Matches 1799; Conserv Query Match 61 61 121 181 241 301 81 301 361 361 421 121 481 541 601 481 54.1 601 ô 셤 ò g g ò a ò ò 8 ŏ Q ò 9 ó q ò a ò g ò 8

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19-JUL-1999;
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18-JUN-1999;
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30-JUN-1999;
01-JUL-1999;
01-JUL-1999;
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13-JUL-1999;
14-JUL-1999;
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Maize histone deacetylase; family 1, ZmHD1; promoter regulator; promoter; Mak polymerase II; transcription; plant transformation; heterochromatin; disease resistance; chromatin assembly; gene activity; toxin screening; pathogenicity; disease response promoter; ds.
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                                                       ggtgttgggtggtgaagggtatactattcgaaatgttgcccgttgctgqtgttatqagac
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                    841 tttccgcagettgtttagacctcttatccagaaggttatggaagtgtatcagccagagge
                                                                                        984 atcagicaagggicacgcigatigcciicggiictiaagaictiacaaggiiccictciat
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altering the levels of heterochromatin, altering chromatin assembly, and gene activity of the transformed plants. Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining
                                                                                                                                                                                                                                                                                            The present sequence encodes a maize histone deacetylase. This DNA belongs to family 1, ZmHD1 and appears to be regulator of promoters for RNA polymerase II, for transcription of genes. The nucleotide sequence can be used to transform plants and increase disease resistance by
                                                                                                                                                                                                                            which have
                                                                                                                                                                                                                                                                                                                                                                                       which disease response promoters are regulated by histone deacetylase.
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/product= "Maize histone deacetylase"
                                                                                                                                                                                                                             transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.1%; Score 614; DB 20; 36.4%; Pred. No. 3e-161; Live 0; Mismatches 370;
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                                                                                                                                                                                                                                                                   Claim 1; Page 46-49; 87pp; English.
                                                                                                                                                            ζ
                                                                                                                                                            Crane
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increased disease resistance
                                                                               99WO-US07370
                                                                                                        98US-0080563
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Best Local Similarity 69.4'
Matches 852; Conservative
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Maize histone deacetylase; family 1, ZmHD1; promoter regulator; promoter; RNA polymerase II; transcription; plant transformation; heterochromatin; disease resistance; chromatin assembly; gene activity; toxin screening;
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The present sequence encodes a maize histone deacetylase. This DNA belongs to family 1, ZmHDl and appears to be regulator of promoters for RNA polymerase II, for transcription of genes. The nucleotide sequence can be used to transform plants and increase disease resistance by altering the levels of heterochromatin, altering chromatin assembly, and gene activity of the transformed plants. Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining which disease response promoters are regulated by histone deacetylase.
                                                                                                                                                                                                     used for producing transgenic plants which have
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 549.6; DB 20;
Pred. No. 2.9e-143;
0; Mismatches 394;
                                                                                                                                                                                                                                              Claim 1; Page 60-63; 87pp; English.
                                                                                                                                Crane VC;
                                                                                                                                                                                                     New deacetylase genes, used increased disease resistance
                                                                                                  (PION-) PIONEER HI-BRED INT
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Best Local Similarity 67.1%;
Matches 828; Conservative
                                          99WO-US07370
                                                                       98US-0080563
                                                                                                                              Briggs SP,
                                                                                                                                                          WPI; 1999-611038/52
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                                                                                                                              Baldwin DA,
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Maize histone deacetylase; family 1, ZmHD1; promoter regulator; promoter; Ma Polymerase II; transcription; plant transformation; heterochromatin; disease resistance; chromatin assembly; gene activity; toxin screening; pathogenicity; disease response promoter; ds.
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/product- "Maize histone deacetylase"
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                                                                                                                                                                                                                                            Claim 1; Page 55-58; 87pp; English.
                                                                                                      Crane VC;
                                                                   (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                             increased disease resistance
99WO-US07370
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Matches 805; Conservative
                                                                                                      Briggs
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                                                                                                                                                                  910 gggcaaggtgatggaggtcttcaaccctggtgcagtcgtgctccagtgtggtgcggattc
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Nucleotide sequence of a histone deacetylase designated AtRPD3A.
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HDA1; ethylene responsive phenotype; hypocotyl elongation;
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The present sequence encodes an Arabidopsis thallana histone deacetylase designated ALRPD3A. The protein is homologous to yeast RPD3 and HDA1. The Polynucleotide sequence is used in the method of the invention. The specification describes a method for regulating gene expression in transgenic plants. The method comprises modifying histones by introducing chimeric nucleotide sequences which have regulatory elements in operative association with a gene of interest or with a nucleotide sequence encoding histone deacetylase. The method is useful for regulating the developmental, physiological or blochemical pathway within a plant, particularly for repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation). The method is also useful as a functional test for identifying a phenotype associated with perturbing a gene. The histone deacetylase genes are useful for altering the development of an organism.
                                                                                                 Methods for regulating gene expression in transgenic plants, e.g. repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation), comprises introducing genes encoding histone deacetylase
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                                                                                                                                                                                       see AAYSBR2B) of rice histone deacetylase 1 (HDI), a chromatin associated protein. The contig was obtained from CDNA clones isolated from rice callus, 15-day old leaf and 15-day-old seedling deacetylases. The invention relates to isolated rice, soybean and wheat nucleic acid fragments encoding HDI. It also relates to the construction of a chimeric gene encoding all or a portion of HDI, in sense or antisense orientation, where expression of the chimeric gene results in production of altered levels of HDI in a remarkormed host cell. The availability of nucleic acid sequences encoding (portions) of histone deacetylase proteins will facilitate studies of global transcriptional regulation in eukaryotic cells,
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                                                                                       New nucleic acid fragment useful as probes and primers, for
                                                                                                                                                                              The present sequence is that of a contig encoding a portion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1990 BP; 502 A; 494 C; 518 G; 476 T; 0 other;
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66.5%;
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                                   New nucleic acid fragment useful as probes and primers, transforming plants
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                                                                                          Claim 3; Page 26-27; 36pp; English.
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AAZ32000 and AAZ32001 encode, and AAY49501 and AAY49502 represent, human metalloprotease thrombospondin (METH) proteins METH1 and METH2
respectively. METH1 and METH2 have been found to be potent inhibitors of angiogenesis both in vitro and in vivo. They can be used for treating cancer and other disorders related to angiogenesis including abnormal wound healing, inflammation, rheumatoid arthitis, psoriasis, endommetrial bleeding disorders, diabetic retinopathy, some forms of macula degeneration, haemangiomas, and arterial-venous malformations. They may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilisation (chemotaxis) of immune cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or toxins), or infectious. They can also be used to treat inflammatory conditions, both chronic and acute conditions. The products can also be used for detection and diagnosis. AAZ32002 to AAY49501 represent sequences given in the exemplification of the present
                                                                                        New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorders
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                                                                                                                                                                                     Disclosure; Page 444-446; 457pp; English
Iruela-Arispe L, Hastings GA,
                                            WPI; 1999-590684/50.
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METH; metalloprotease; thrombospondin; anglogenesis inhibition; cancer therapy; benign tumour; ocular anglogenic disease; rheumatoid arthritis; psoriasis; wound healing; endometriosis; vasculogenesis; granulation; hypertrophic scar; nonunion fracture; scleroderma, trachoma; vascular adhesion; myocardial anglogenesis; coronary collateral; cerebral collateral; arteriovenous malformation; ischaemic limb anglogenesis; osler-Webber syndrome; wound granulation; plaque neovascularisation; telanglectasia; haemophiliac joint; EST; anglofibroma; fibromuscular dysplasia; expressed sequence tag; crohn's disease; atherosclerosis; birth control; ss.
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The present invention relates to human METH1 and METH2, (ME for metalloprotease and TH for thrombospondin; see AAB50002 and AAB50003). The present sequence is an expressed sequence tag (EST) for METH. WETH can be used for inhibiting applogenesis in an individual, and for treating cancer, benign tumours, an ocular angiogenic disease, rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars, nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, coronary collaterals, cerebral collaterals, arteriovenous malformations,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ischemic limb angiogenesis, Osler-Webber syndrome, plaque neovascularisation, telanglectasia, haemophiliac johnts, angiofibroma, fibromuscular dysplasia, wound granulation, Crohn's disease or atherosclerosis. METH can also be used in birth control. METH can also be used in diagnostic methods for the prognosis of cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                            METHI and METH2 polynucleotides and encoded polypeptides, used to inhibit angiogensis in the treatment of disorders such as cancer, rheumatoid arthritis and psorlasis -
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                                                                                                                                                             BETH ISRAEL DEACONESS MEDICAL CENT. IRUELA-ARISPE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 14; Pages 745-746; 768pp; English.
                                                                                                                                            SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                           Hastings GA,
            99US-01448B2,
99US-0147823,
99US-0373658,
99US-0171503,
                                                                                                                            HUMAN GENOME SCI INC
                                                                                       2000US-0183792
                                                                                                                                                                                                                                                                                                                   Iruela-Arispe L, Hasting:
                                                                                                                                                                                                               RUBEN S M.
JONAK Z L.
TRULLI S H.
FORNWALD J A.
                                                                                                                                                                                                HASTINGS G A.
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                                                                                                                                                                                                                                                                                                                                             Fornwald JA,
                                                                                       22-FEB-2000;
              20-JUL-1999;
10-AUG-1999;
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22-DEC-1999;
                                                                                                                                           (SMIK)
(BETH-)
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                             594 tgatatggctgttaattgggctggaggattacatcatgctaagaaatacgaagcatcagg
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enzyme activity. These inhibitors are useful for treating cancers and for identifying which histone deacetylase is involved in a neoplasia.
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                                                                                                                                                                                                                                                                 Antisense oligonucleotide that inhibits expression of a histone deacetylase, useful for treating and/or alleviating the symptoms neoplasia, or for inhibiting neoplastic cell growth in an animal
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Pred. No. 6.2e-114;
0; Mismatches 454;
                                                                                                                                                                                                                                                                                                                              Disclosure; Page 53; 125pp; English.
                                                                                                                                                                                      Besterman JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 24.7%;
Best Local Similarity 61.4%;
Matches 733; Conservative
                                                                                         03-MAY-2000; 2000WO-IB01252.
                                                                                                                       99US-0132287
                                                                                                                                                                                                                    WPI; 2001-016407/02
                                                                                                                                                      (METH-) METHYLGENE
                                                                                                                                                                                      Macleod AR, Li Z,
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                            WO200071703-A2
                                                                                                                       03-MAY-1999;
Homo sapiens
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Maize histone deacetylase; family 1, ZmHD1; promoter regulator; promoter; RNA polymerase II; transcription; plant transformation; heterochromatin; disease resistance; chromatin assembly; gene activity; toxin screening;
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/product= "Maize histone deacetylase"
                                                                                                                                                                                                                           pathogenicity; disease response promoter; ds.
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The present sequence encodes a maize histone deacetylase. This DNA belongs to family 1, ZmHD1 and appears to be requiator of promoters for RNA polymerase II, for transcription of genes. The nucleotide sequence can be used to transform plants and increase disease resistance by altering the levels of heterochromatin, altering chromatin assembly, and gene activity of the transformed plants. Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining which disease response promoters are regulated by histone deacetylase.
                                                                                                                          for producing transgenic plants which have
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                                                                                                                                                                                                                                                                                                                                                                Length 1475;
                                                                                                                                                                                                                                                                                                                                                             Score 441.4; DB 20; Length
Pred. No. 4.2e-113;
0; Mismatches 226; Indels
                                                                                                                                                                                                                                                                                                                    Sequence 1475 BP; 388 A; 342 C; 376 G; 369 T; 0 other;
                                                                                                                                                                Claim 1; Page 51-53; 87pp; English.
                                                     ζ
                         (PION-) PIONEER HI-BRED INT INC.
                                                      Crane
                                                                                                                                       increased disease resistance
                                                                                                                                                                                                                                                                                                                                                             Query Match 24.5%;
Best Local Similarity 71.9%;
Matches 577; Conservative
                                                                                                                         nsed
98US-0080563
                                                     Briggs SP,
                                                                                                                         deacetylase genes,
                                                                                WPI; 1999-611038/52
                                                                                             P-PSDB; AAY28798
03-APR-1998;
                                                     Baldwin DA,
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The present cDNA sequence encodes a novel histone deacetylase (HDx) polypeptide, designated HDI. The HDx polypeptides are capable of modulating proliferation survival and differentiation of cells. The proteins are able to alter chromatin structure by deacetylating histones such as H3 or H4. They have the ability to modulate cell growth by influencing cell cycle progression or to modulate gene transcription. The products can be used for diagnosis and therapy. They can be used, for example, to treat tumours or proliferative disorders or spermatogenesis, osteogenesis, chondrogenesis or the differentiation of progenitor cells. They can also be used to treat psorlasis, bone diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fibroproliferative disorders, degenerative disorders, or for repair of cartilage, increasing bone density, liver repair subsequent to a partial hepatectomy, to promote regeneration of lung tissue in the treatment of emphysema, or for inducing tolerance in autoimmune diseases, and transplant recipients. Hox inhibitors can be used as anti-fungal agents, preservatives in foodstuff, feed supplements for promoting weight gain in livestock, disinfectants, insecticides or defoliants. The products can
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Histone deacetylase gene; HDx; HDI; HDx polypeptide; deacetylation; H3; H4; cell differentiation; chromatin structure; cell cycle progression; proliferative disorder; fibroproliferative disorder; fibroproliferative disorder; autoimmune disease; HDx inhibitor; ss.
                                                                             1290 cgtccagtttcagcacaccaccagtcaatcgagttttggacgagccggaagatgacat 1349
                                                                                                                  880 cactcaattccatgacagaccgtcagaccttgaagctccagaggagaaagaggagacat 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated histone deacetylase polypeptide(s) and genes - used to develop products for modulating the proliferation, survival or differentiation of cells, e.g. for treating tumours.
1230 tatggagagagataaggaacacgttgctggaacaactttcgggactaatacacgcacctag
                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA encoding a histone deacetylase (HDx) protein, designated HD1.
                                     820 cttggagaacataaagaacatgatattggagaacctgtcaaagatagaacatgttcccag
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                                                                            Score 438.2; DB 18; Length 1449;
Pred. No. 3.3e-112;
0; Mismatches 418; Indels 6;
                                Sequence 1449 BP; 406 A; 329 C; 396 G; 318 T; 0 other;
also be used in cell cultures
                                                                                  Query Match 24.3%;
Best Local Similarity 62.4%;
Matches 705; Conservative (
                                                                                                                                                                                                                                                                                                294
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1038 teetteeaatatgaetaaceagaacaegaatgagtaeetggagaagateaaaeagegaet 1097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                  Histone deacetylase; HDAC-1; HDAC-2; HDAC-4; HDAC-5; HDAC-C; HDAC-C; HDAC-D; cell cycle; tumourigenesis; cancer; inhibitor; antisense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        jo .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense oligonucleotide that inhibits expression of a histone deacetylase, useful for treating and/or alleviating the symptoms neoplasia, or for inhibiting neoplastic cell growth in an animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 1611;
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                                                                                                                          gotggaacaactttcgggactaatacacgcacctagcgtccagtttcag 1302
                                                                                                                                        Indels
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US-09-645-337-3 1800 Title: Perfect score:

1 gigcccacaactcctagtaa.....acgcgigcaigcgacgicai 1800 Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Searched:

Total number of hits satisfying chosen parameters:

351203 seqs, 113238999 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8	184	10.2	841	4	US-08-998-416-317	317
6	75	4.2	2581	7	US-09-013-634-1	1,
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14	68	3.8	2460	4	US-08-964-127-1	ı,
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7	49.4	2.7	3327	m	US-08-689-421-26	26,
c 25	4.64	2.7	3327	4	US-09-389-528-26	26,
c 23	4.64	2.7	3327	4	US-09-181-827A-26	Sequence 26, Appl
24	49	2.7	2815	m	US-09-214-564A-1	Sequence 1, Appli
25	48.8	2.7	2205	m	US-08-888-077A-41	41,
26	44.4	2.5	2295	a	US-08-842-842-6	Sequence 6, Appli
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4 US-08-885-469-1 2 US-08-920-234-1 1 US-07-882-292-1 2 US-08-31-644-1 5 PCT-US93-04102-1 3 US-08-945-950-11 3 US-08-946-951-1 4 US-09-193-069-1 4 US-09-193-069-1 5 PCT-US92-10087-16 5 PCT-US92-10087-16 5 US-08-330-108-16 5 US-08-330-108-16 6 US-08-330-108-16 7 US-08-330-108-16 8 US-09-33-300-6 9 US-09-31-300-6 1 US-07-779-890-3	ULT 1 1	%; Score 614; DB 4; %; Pred. No. 5.2e-16 0; Mismatches 37 cggacgtaagcgggggtcag
2.4 3349 2.3 28830 2.3 28830 2.3 28830 2.3 28830 2.2 3 12921 2.2 1074 2.2 1198 2.2 2 2047 2.1 14507 2.1 14507 2.1 2218	SULT 1 SULT 1 Sequence 1, Application US/09282305 Patent No. 6287843 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Briggs, Steven P. APPLICANT: Briggs, Steven P. APPLICANT: Briggs, Steven P. APPLICANT: US OF TITLE OF INVENTION: Maize Histone Dear FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282, CURRENT APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1999-03-31 PRIOR FILING DATE: 1999-04-03 PRIOR FILING DATE: 1998-04-03 PRIOR FILING DATE: 1998-04-03 CURRENT FILING DATE: 1998-04-03 PRIOR FILING DATE: 1998-04-03 PRIOR FILING DATE: 1998-04-03 CURRENT: BALOR FILING DATE: 1998-04-03 PRIOR FILING DATE: 1998-04-03	Match Local Similarity 69.4% Local Similarity
29	RESULT US-09-282-305-1 DS-09-282-305-1 Patent No. 6287843 GENERAL INFORMATION: APPLICANT: Briggs, S APPLICANT: Crane, VI TILLE REFERENCE: 5718 CURRENT FILING DATE: 1 PRIOR APPLICATION NUM PRIOR FILING DATE: 1 PRIOR FILING DATE: 1 PRIOR FILING DATE: 1 NUMBER OF SEQ ID NOS: SOFTWARE: Patentin V SEQ ID NO I LENGTH: 1826 LENGTH: 18	Ouery Ma Query Ma Best Loc Matches y 145 b 62 b 122 y 265 y 265

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RESULT 2
US-09-282-305-7
Sequence 7, Application US/09282305
Fatent No. 6287843
GENERAL INFORMATION:
APPLICANT: Baldwin, Donald A.
APPLICANT: Crane, Virginia C.
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126 ggcagacgaaagcggcatctctctccgccgtc---gggacccgacggacgtaagcggcgagt 182
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TITLE OF INVENTION: Maize Histone Deacetylases And Their
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                                                                                                                                                                                                                                                                                                                          0; Mismatches 394;
                                                                                                                                                                                                                                                                                          30.5%; Score 549.6; DB 4; 67.1%; Pred. No. 1.4e-147;
   FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/080,563
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                          Matches 828; Conservative
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: LOCATION: (57)..(1610)
US-09-282-305-7
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Pred. No. 5.2e-142;
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; LOCATION: (140)..(1459)
US-09-282-305-5
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Matches 805; Conserv
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                                                                     APPLICANT: Baldwin, Donald A.
APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: US/09/282,305
PRIOR TRIING DATE: 1999-03-31
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 24.5%; Score 441.4; DB 4;
Best Local Similarity 71.9%; Pred. No. 1.1e-116;
Matches 577; Conservative 0; Mismatches 226;
                 Sequence 3, Application US/09282305
Patent No. 6287843
GENERAL INFORMATION:
                                                                                                                                                                                                                                                               Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: (29)..(1084)
US-09-282-305-3
                                                                                                                                                                                                                                                                                                                                 ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                  1475
US-09-282-305-3
                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                               SEQ ID NO 3
                                                                                                                                                                                                                                                               SOFTWARE:
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1170 eccagattataegetteatgtegacecaagteetatggagaatttaaacaegeeeaaaga 1229
                                                                              760 ccctgattatactcttcatatccaaccaaaagtgttgaaaacctgaataccacaaagga
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MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IDEM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA: US/08/528,255A
FILING DATE: September 14, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: human fetal lung cDNA library
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TITLE OF INVENTION: RPDL PROTEIN AND I
TITLE OF INVENTION: ENCODING THE SAME
                                                                                                                                                                                                                                                 1350 ggagacaagaccaaaacctcgca 1372
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: J96-227876
FILING DATE: 22-SEPTEMBER-1994
APPLICATION NUMBER: J77-183763
                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 2, Application US/08528255A
; Patent No. 5659016
                                                                                                                                                                                                                                                                                         940 ggacaagaggccacctcagcgca 962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: NAKAMURA, YUSUKE APPLICANT: FURUKAWA, YOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 20-JULY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INPORMATION FOR SED ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA to mRNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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DENTIFICATION METHOD: US-08-528-255A-2
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CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, TH
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STATE: Michigan
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US-08-528-255A-2
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TITLE OF INVENTION: RPDL PROTEIN AND
TITLE OF INVENTION: ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/528 255
FILLING DATE: September 14, 1995
APPLICATION NUMBER: JP6-227876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 22-SEPTEMBER-1994
APPLICATION NUMBER: JP7-183763
FILING DATE: 20-JULY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                        US-08-717-365-2; Sequence 2, Application US/08717365; Patent No. 5763182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Terryence F. Chapman REGISTRATION NUMBER: 32549
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TELEFAX: (616) 381-5465
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
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N: 536
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                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: Septem APPLICATION NUMBER: FILING DATE: 22-SEP
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STRANDEDNESS: doub
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STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                              Michigan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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                                                                                                                                                                                                          294 ccgtcgcttagaaatcagtcgccctagcctcgctgacgcctccgatatcggccgattcca 353
                                                                                                                                                                                                                                381 GTTTGAGTTCTGTCAGTTGTCTACTGGTGGTTCTGTGGCAAGTGCTGGAAACTTAATAA 440
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                                      Gaps
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 Length 2111;
                                 Indels
24.2%; Score 435; DB 1; I 62.3%; Pred. No. 9.2e-115; Ive 0; Mismatches 420;
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                                                                                                                                                                  MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage COMPUTER: IBM PC/XI/AT Compatible OPERATING SYSTEM: MS-DOS 5.0 SOFTWARE: OWOTGPETCH 5.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,365
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Pred. No. 9.2e-115;
0; Mismatches 420;
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS, P.C. STREET: 2026 Rambling Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: Furuya Case 1335 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                APPLICANT: Baldwin, Donald A.
APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: U$/09/282,305
CURRENT FILING DATE: 1999-03-31
PRIOR PILLING DATE: 1998-04-03
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Pred. No. 1.4e-96;
                                        ; Sequence 9, Application US/09282305
; Patent No. 6287843
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Best Local Similarity 59.0%;
Matches 678; Conservative 0
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SOFTWARE: Patentin Ver. 2.0
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US-09-282-305-9
                                                                                                                                 GENERAL INFORMATION:
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JS-09-282-305-9
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ATTORNEY/AGENT INFORMATION:

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1103 ctgcagttgctgttggagtagagccggacaacaccccttacaatgagtattttgagt 1162
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                                                                                                                                                                                                                      983 tatcagicaagggicacgcigatigecticggitetiaagaictiacaacgitecietea 1042
                                                                                                                                                                                                                                                                                                             1043 tggtgttgggtggtgaagggtatactattcgaaatgttgcccgttgctggtgttatgaga 1102
                                                                                                                              861 tetetattgaaggecatgetgaatgtgtaaagtttgteaagaaatteaatatteeette 920
681 aaagggaaggaaaatattatgctatcaacattccacttaaagatgggatagatgacacta 740
                                         863 gtttccgcagcttgtttagacctcttatccagaaggttatggaagtgtatcagccagagg
                                                                                     741 getttaeteggeettttaaaacaattattgeeaagttgttgagacatatetgeetggtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1223 ccaaagatatggagagagataaggaacacgttgctggaacaactttcgggactaatacacg
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TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 317, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
Mohr, Christine
Wendland, Jurgen
Knechtle, Philipp
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   673 atagatattgatgtccaccatggagatggagtggaagaagaggttttacaccactgataga 732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 ATCGATGATGATTCGTACATCAACTTATTTAAGAGCATCATAGACCCGCTAGTTACATCA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 TACAAGCCAACAGTAATTATTCAGCAATGTGGAGCAGACTCTTTGGGGCATGACAGACTG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               553 atcaattgggggggggtgggcttcaccatgctaagaaaagcgaggcttctgggttttgctat 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 GATGAGATGGGATGCTCGCGGGGCAAGCACTTTTCGCTGAATGTGCCGCTCAATGACGGC 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      850 atggacgatgaaagtttccgcagcttgtttagacctcttatccagaaggttatggaagtg 909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    613 gtaaacgacatcgtgctagggattctggagttgctcaagatgtttaagcgggttctctac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       910 tatcagccagaggcagttgttcttcagtgtggtgctgactccttaagtggtgatcggttg
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APPLICANT: M. Alexandra Glucksmann and Keith Robison
TITLE OF INVENTION: LIGAND RECEPTORS AND USES THEREFOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                             Score 184; DB 4; L
Pred. No. 3.8e-43;
0; Mismatches 215;
                                         PF/5-30306/A/CGC1976
                              REFERENCE/DOCKET NUMBER: PF/S
TELECOMMUNICATION INFORMATION:
TELEFAN: 919-541-8689
INFORMATION FOR SEQ ID NO: 317:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09013634 Patent No. 5945307
                 38,241
                                                                                                                                                                                                              MOLECULE TYPE: DINA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                               10.2%;
60.6%;
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1090 tggtgttatgagactg 1105
                                                                                                                                                                LENGTH: 841 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    541 TGGACGTACGAGACAG 556
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Matches 337; Conservative
                                                                                                                                                                                                                                                                                          ; ORGANISM: PAG1256UP
US-08-998-416-317
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APPLICANT: Wang, Hongyu
APPLICANT: Wang, Hongyu
APPLICANT: Wang, Larry R.
APPLICANT: Wang, Larry R.
APPLICANT: Wang, Mang, Mang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 4.2%; Score 75; DB 2; Length 2581; Best Local Similarity 100.0%; Pred. No. 1e-11; Matches 75; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Attorney, Jean M. Silveri
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MI-036
TELECOMMUNICATION INFORMATION:
TELEPAX: (617)227-7400
TELEPAX: (617)227-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-118-442-29/c
; Sequence 29, Application US/09118442B
; Patent No. 6197561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2581 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2557 TGCATGCGACGTCAT 2571
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                                                                                                                             Massachusetts: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 184..1194
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                                                                                      Boston
                                                                                                                                                                                                       02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
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                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-013-634-1
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APPLICANT: Martino-Catt, Susan J.
APPLICANT: Martino-Catt, Susan J.
APPLICANT: Marty Hongy
PAPPLICANT: Marty Hongy
TITLE OF INVENTION: Genes Controlling Phytate Metabolism in
TITLE OF INVENTION: Darry R.
TITLE OF INVENTION: Plants and Uses Thereof
FILE REFERENCE: 0706D
CURRENT APPLICATION NUMBER: US/09/677,064
CURRENT APPLICATION NUMBER: 60/055,446
PRIOR FILING DATE: 1997-08-11
PRIOR FILING DATE: 1997-08-18
PRIOR FILING DATE: 1997-08-18
PRIOR FILING DATE: 1997-07-28
PRIOR FILING DATE: 1997-07-28
PRIOR FILING DATE: 1998-07-17
NUMBER: OF SEQ ID NOS: 31
NUMBER: OF SEQ ID NOS: 31
NUMBER: FEATFOR EASTER OF SEQ ID NOS: 31
                                                                                                                                                                           Query Match 4.0%; Score 72; DB 4; Length 1330; Best Local Similarity 100.0%; Pred. No. 5.3e-11; Matches 72; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 4.0%; Score 72; DB 4; Length 1330; Best Local Similarity 100.0%; Pred. No. 5.3e-11; Matches 72; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 29 LENGTH: 1330
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-09-677-064-29/c
: Sequence 29, Application US/09677064
: Patent No. 6291224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08383756
Patent No. 5654495
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APPLICANT: Debesh, Katayoon
APPLICANT: Voelker, Toni Alois
APPLICANT: Hawkins, Deborah
APPLICANT: Davies, Huw Maelor
                                                                                                                                                                                                                                                                                                                                                 1789 atgcgacgtcat 1800
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                                                             ; TYPE: DNA
; ORGANISM: Zea mays
US-09-118-442-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Zea mays
US-09-677-064-29
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Pred. No. 6.2e-10;
0; Mismatches 6; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Production of Myristate in Plant Cells
IITLE OF INVENTION: Production of Myristate in Plant Cells
                                                                                                                                                                          COMPUTER REALBABLE FORM
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1(a)
SOFTWARE: Microsoft Word 5.1(a)
SOFTWARE: Microsoft Word 5.1(a)
SOFTWARE: Microsoft Word 5.1(a)
APPLICATION NUMBER: US/08/383,756
FILING DATE: 0.2-FEB-1995
CLASSIFICATION DATA:
APPLICATION WORDER: 08/261,695
FILING DATE: 16-UN-94
CLASSIFICATION ATA:
APPLICATION NUMBER: PCT/US93/10814
FILING DATE: 29-OCT-93
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US93/10814
FILING DATE: 30-OCT-93
CLASSIFICATION DATA:
APPLICATION NUMBER: USSN 07/968,971
FILING DATE: 30-OCT-92
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGNE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08460898
Patent No. 5850022
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dehesh, Katayoon
APPLICANT: VOELKEr, Toni Alois
APPLICANT: HAWKINS, DEDOCAH
APPLICANT: DAVIES, HUW MORDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: CDNA to mRNA
US-08-383-756-1
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Best Local Similarity 92.3%;
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oy 1783 gcgtgcatgcgacgtcat 1800
               NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1581 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
EDNESS: double
                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                           SIL.
CITY: L.
STATE: CA
COUNTRY: USA
TO: 95616
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1468 GTCATTAAGTTAAAAAAAAAAAAAGGGCGGCCGCTCTAGAGGATCCAAGCTTACGTAC 1527
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Sequence 1, Application US/08964127

Patent No. 6277565

GENERAL INFORMATION:

APPLICANT: Grandearl, Andrew David John

ITLE OF INVENTION: NOVEL GENES ENCODING TRANSPORTER-LIKE
                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKT NUMBER: GGNE 111-1
TELECOMUNICATION INFORMATION:
TELEPAN: (916) 753-6313
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1581 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

SOFTWARE:

MICROSOFT WOOD 5.1(a)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/460,898

FILING DATE: 05-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: 08/383,756

FILING DATE: 05-FEB-1995

CLASSIFICATION: 435

PRIOR APPLICATION UNMBER: 08/261,695

FILING DATE: 16-JUN-94

CLASSIFICATION UNMBER: PCT/US93/10814

FILING DATE: 29-OCT-93

CLASSIFICATION: 435

PRIOR APPLICATION UNMBER: PCT/US93/10814

FILING DATE: 39-OCT-93

CLASSIFICATION ATS

APPLICATION DATA:

APPLICATION NUMBER: 19-OCT-92

ATOORNEY/AGENT INFORMATION:

NAME: ELIZABETH LASSEN

NAME: ELIZABETH LASSEN

NAME: FLORMER F SCHAFOR

NAME: FLORMER F SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USSN 07/968,971
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MOLECULE TYPE: cDNA to mRNA
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                                                            ADDRESSEE: Calycon.
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REGISTRATION NUMBER: 34
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                     95616
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APPLICANT: Martino-Catt, Susan J.
APPLICANT: Wang, Hongyu
APPLICANT: Wang, Hongyu
APPLICANT: Wang, Xun
APPLICANT: Bowen, Benjamin A.
TITLE OF INVENTION: Genes Controlling Phytate Metabolism in
TITLE OF INVENTION: Genes Controlling Phytate Metabolism in
TITLE OF INVENTION: Blants and Uses Thereof
FILE REFERENCE: 0706
CURRENT APPLICATION NUMBER: 05/09/118,442B
CURRENT PILLING DATE: 1998-07-17
EARLIER FILING DATE: 1998-07-17
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-08
EARLIER FILING DATE: 1997-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 3.8%; Score 68; DB 4; Length 2460; Best Local Similarity 100.0%; Pred. No. 1e-09; Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                         COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
FILING DATE: 06-NOV-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Crews, Ph.D., L. Lee
REGISTRATION NUMBER: P-43.567
REFERENCE/DOCKET NUMBER: 07334/038001
TELECOMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPRAK: 617/542-8076
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-09-118-442-31
: Sequence 31, Application US/09118442B
: Patent No. 6197561
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2460 base pairs
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                                                                                                                                                       COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKELLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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US-09-645-337-3
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                   OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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em_gss_fun:*
em_gss_hum:*
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em_gss_rod:*
em_gss_vrt:*
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Maximum DB seq length: 200000000
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em_htc:*
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			•			SUMMAKIES	
Res	Result		% Ouery				
;	No.	Score	Match	Match Length DB	DB	ID	Description
U	-	809			10	AV560183	AV560183 AV560183
	7	509.2			10	AI994522	AI994522 701498504
	m	428.8	23.8		11	B1177518	BI177518 EST518463
O	4	380.8	21.2		10	AV567115	AV567115 AV567115
	'n	365	20.3		10	AJ394397	AJ394397 AJ394397
	9	353	19.6		10	AL518877	AL518877 AL518877
	7	347.2	19.3		13	CNS072YS	AL426842 clone BA0
υ	80	347	19.3	907	13	CNSO6TIS	AL414998 T3 end of
	6	343.4	19.1		10	AI726977	A1726977 BNLGH1702
ပ	10	342.2	19.0	_	13	CNS06MLI	AL405628 T3 end of
	11	341	18.9		11	BF324960	BF324960 su29e12.y
	13	340.2	18.9		10	AL531607	

AM217600 EST296314 AA394745 26542 Lam AL558916 AL558916 BE036429 MODT000 BE036429 MODT00100 BE176911 BE17691	Avs60183.1 G1:8731609 EST. EST. Arabidopsis thaliana Eukaryota: Viridiplantae: Streptophyta; Embryophyta: Tracheophyta; Enkaryota: Viridiplantae: Streptophyta; Embryophyta: Tracheophyta; Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae: eurosids II: Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 609) Asamizu.E., Nakamura,Y., Sato,S. and Tabata,S. A large scale analysis of CDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized an size-selected cDNA libraries DNA Res. 7, 175-180 (2000) 20653093 Contact: Erika Asamizu The First Laboratory for Plant Gene Research Kazusa DNA Research Institute Yana 153-3; Klasarau, Chiba 292-0812, Japan Email: asamizu@kazusa. Chiba 292-0812, Japan Email: asamizu@kazusa. Chiba 292-0812, Japan First Laboratory for Plant Gene Research Yana 153-3; Klasarau, Chiba 292-0812, Japan First Laboratory for Plant Gene Research Actain-Countingalifiers 1.609 /organism-Arabidopsis thaliana /strain-Colome-Ispe-Euxon:3702" /clone-Ispe-Marbidopsis thaliana green siliques Columbia* /tissue_type="green siliques" /tissue_type="green siliques" /note="vector: pBluescriptII SK-: Site_1: EcoRI; Site_2: Xhol: Xhol:
AW217600 AA394745 BL558916 BEG58916 BG749764 BG756668 AU132519 AU32519 AU555361 AL555361 AL555361 AL555361 AL555361 AL555361 AL555361 AU308961 AU308074796 BG74796 BG914796 BG914796 BG914796 BG755703 BG755703 BG755703 BG755703 BG755703 BC75703 BC75703 BC75703 BC7797	ess. bit didiplana a: Viridiplana a: Viridiplana bphyta: Magnoliophyta; eudicotyl pphyta: Magnoliophyta; eudicotyl pphyta: Magnoliophyta; eudicotyl selvosids II; Brassicales; Bras sel to 609) Brassicales; Bras scale analysis of cDNA in Arabi 8 nor-redundant expressed seque tected cDNA libraries 7, 175-180 (2000) st Laboratory for plant Gene Res NNA Research Institute NNA Research Institute SNA Rasarau, Chiba 292-0812, samizu@kazusa.or jp, URL:http:/ Location/Qualifiers 1. 609 /clone=*Sol30file* /clone=*Sol30file* /clone=*Sol30file* /fissue_type="green sliques" /note="Vector: pBluescriptII S /note="Vector: pBluescriptII S /note="Vector: pBluescriptII S
621 10 8431 10 8447 10 9467 10 9467 10 947 10 910 11 7 8898 10 917 11 8 918 10 2 917 11 8 918 10 9 917 11 1 107 13 1 107 1	ress. psis thaliana tray Viridiplantae; tophyta; Magnolioph, eurosids II; Bra eurosids II; Bra ellos 10 609) tophyta; Magnolioph scale analysis of 28 non-redundant elected cDNA librar. 7, 175-180 (2000) 3. Erika Asamizu. Alsarazu. bNA Research Insti 32-3, Kisarazu. Corganism="Rolumbi / Alb xref="texon: / Alb xref="texon: / Clone_lib="Arabi / Alsare_lib="Arabi
18.65 18.65 18.65 18.65 18.65 18.65 19.65	Av560183.1 G1:8731609 EST. Arabidopsis thaliana Eukaryota; Viridiplantae; S: Spermatophyta: Magnoliophyt Rosidae; eurosids II; Brass, 1 (bases 1 to 609) Asamizu,E., Nakamura,Y., Sa' A large scale analysis of Ci of 12.028 nor-redundant exp size-selected cDNA libralee Contact: Erika Asamizu Contact: Frie Colubia Yana 1532-3, Klastazu, Chib Email: asamizu@kazusa or.jp Cotation/Qualifier 1.609 //clone="Sq130f11F" //clone="Sq130f11F" //clone="Sq130f11F" //clone="laxon:37 //db xref="taxon:37 //db xref="taxon:37 //clone="sq130f11F" //clone="laxon:37 //clone="laxon
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Chen, J., Mondyama, M., Chan, E., Mooney, M., Carroon, B., Gillilland, D., Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P., Gorgone, G., Burns, D., Griffin, J., Mouancutoua, M., Nguyen, D., Tan, R., Roselm, Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Murry, L., Turner, C., Krikorian, S., Elder, L. and Hanson, D.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
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A1994522
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                                                                                                                                                                            1141 cettacaatgagtattttgagtatttcggcccagattatacgettcatgtcgacccaagt 1200
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                                                           Score 608; DB 10;
Pred. No. 2.3e-100;
0; Mismatches 1;
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    б
   129
                                                         33.8%;
99.8%;
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                                                                                      Matches 608; Conservative
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/organism-"Arabidopsis thaliana"
/db_xref-"taxon:3702"
/db_xref-"taxon:3702"
/clone="701498504"
/clone="10-"A. thaliana, Obio State clone set"
/note-"cDNA library was made from selected clones from the Arabidopsis thaliana Obio State clone set."
a 129 c 141 g 158 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DALI//518 737 bp mRNA EST 09-JUL-2001 EST518463 CSTE Solanum tuberosum cDNA clone cSTE10D9 5' sequence, BI177518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           433 cgattcaatgtcggtgaggattgtcctgtcttcgacggactttttgatttttgccgtgct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 613 gtaaacgacatcgtgctagggattctggagttgctcaagatgtttaagcgggttctcac
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                                                     of Incyte
                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                           28.3%; Score 509.2; DB 10; Length 553; 97.1%; Pred. No. 1.6e-82; live 0; Mismatches 13; Indels 3;
                                                                                    4633 World Parkway Circle, St. Louis, MO 63134, USA
Tel: 877-577-2733
                                                   subsidiary
Arabidopsis thaliana Gene Expression MicroArray Unpublished (1999)
Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary Pharmaceuticals, Inc.
                                                                                                                                         Email: service@genomesystems.com
                                                                                                                                                          Location/Qualifiers
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                                                                                                                      Fax: 314-427-3324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gacgatgaaagtttcc
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/note-"Vector: pBluescript SK(-); Site_1: ECORI; Site_2:
Xho1: Tissue supplied by Christian Bachem and Richard
Visser (Department of Plant Breeding, wageningen
University, The Netherlands). The cSTA libraries will
attempt to capture the induction and initiation/initial
growth of the tuber in an in vitro system as described in
Bachem et al. (Plant Journal, 1996). Small microtubers
develop from axillary buds attached to stem explants when
placed on a high sucrose medium (10%). Visible
morphological changes occur synchronously at day five in
the axillary buds. The first library, cSTA (1-20) consists
of axillary buds harvested on days 1-3. This targets
those genes involved in induction of the microtubers. The
following libraries, cSTA (21-40) and cSTA (41-60),
capture genes involved in tuber initiation and outgrowth.
This library is noted as p3 in Tanksley lab notebooks."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
                                                                                                                                  Asteridae, euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 737)
van der Hoeven, R., Bezzerides, J., Bachem, C., Visser, R., Cho, J.,
Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             608 gctatgtaaacgacatcgtgctagggattctggagttgctcaagatgtttaagcgggttc 667
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                                                                                                                                                                                                                                                                                                    Unpublished (2001)
Contact: Cathy Ronning
The Institute for Genomic Research
For clone Info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GCTATGTGAATGATATTGTTCTTGGTATTCTTGAGCTCCTCAAAGTCCACAAGCGTGTGT
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                                                                                                                                                                                                                                                                          Generation of ESTs from in vitro grown microtubers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="7, 8 and 10 days"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Solanum tuberosum"
/cultivar="Bintje"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4113"
/clone="cSTE10D9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: Ml3F-R.
                          potato.
Solanum tuberosum
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1 (bases 1 to 387).
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res, 7, 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The First Laboratory for Plant Gene Research Kazusa DNA Research Institute Yana 1532-3, Klsarazu, Chiba 292-0812, Japan Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Arabidopsis thaliana green siliques Columbia"/tissue_type="green siliques"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV567115 385 bp mRNA EST 07-SEP-2000 AV567115 Arabidopsis thaliana green siliques Columbia Arabidopsis thaliana cDNA clone SQL07b02F 3', mRNA sequence.
AV567115
                                                                                                                           1088 gctggtgttatgagactgcagttgctgttggagtagagccggacaacaaactcccttaca 1147
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361 TGGGTTGCTTCAACTTGTCTGTCAAGGGCCATGCCGCTTGCCTTAGGTACCTCAGAICCT 420
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                                                                                                                                                                                                                           tgggttgcttcaacttatcagtcaaggtcacgctgattgccttcggttcttaagatctt
                                                                                                                                                                                                                                                                                               Score 380.8; DB 10; Length 385; Pred. No. 2.9e-59;

    .385
    /organism="Arabidopsis thaliana"

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/db_xref="taxon:3702"
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A large database of chicken bursal ESTs as a resource for the analysis of vertebrate gene function
Genome Res. 10 (12), 2062-2069 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves, Neognathae; Galliformes; Phasianidae;
Phasianinee; Gallus.
1 (bases 1 to 765)
                                                                                                                                                                                                                                                                                                                                                                                                 gallus cDNA clone 19d16rl, mRNA sequence
                       gatgatgataaaacctcttcatggttactcatgtcgtggtggcgcaactacggacagggac 1470
                                                                                                                                                               tctaccggtgaagatgaaatggatgacgataacccagagccagacgtgaatcctccatcg 1530
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Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
1. 765
                                                                                                                            TCTACCGGTGAAGATGAAATGGATGACGATAACCCAGAGCCAGACGTGAATCCTCCATCG
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120 c 189 g 242 t
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68.6%; Pred. No. 1.6e-56;
  Mismatches
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/clone-"19d16r1"
/clone_lib-"dkf2426"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [Libaes] to 999)
Libaes; Toruber, C., Jessee, J. and Polayes, D. Full-length CDNA libraries and normalization
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                                         125 TTAATTGGGCTGGAGGACTTCACCATGCCAAGAAGTCAGAGGCATCTGGTTTTGTTATG 184
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BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
5 GATTTAATGTTGGAGAAGATTGTCCTGTATTTGATGGCCTGTTTGAGTTTTGTCAGCTGT
                                                                                                                             554 tcaattgggggggggttcaccatgctaagaaaagcgaggcttctgggttttgctatg
                                                                                                                                                                                                                    614 taaacgacatcgtgctagggattctggagttgctcaagatgtttaagcgggttctctaca
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/note-"Organ: brain; Vector: pCMVSPORT 6: 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville , Maryland 20856, USA Fax: (1) 301 610 8371 Email: fliangelifetech.com URL: http://fulllength.invitrogen.com" 10 others
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                                                                                             /tissue_type="neuroblastoma cells"
/lab_host="DH108"
                                                      /clone_lib="LTI_NFL011_NBC1"
/sex="male"
/organism-"Homo sapiens"
                                      /clone-"CS0DA011YG11"
                    /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 62.6 Matches 592; Conservative
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Direct Submission

Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:

seqref(genoscope.cns.fr - Web: www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
candida tropicalis and farrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                   .013 ggttettaagatettaeaaegtteeteteatggtgttgggtggtgaagggtataetatte 1072
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                                                                                                            954 aagt-ggtgatcggttgggttgcttcaacttatcagtcaagggtcacgctgattgccttc
                                                                                                                                         894 gaaggttatggaagtgtatcagccagaggcagttgttcttcagtggtggtgctgactcctt
                            880 AATITGTCAAGAGCTTTAACCTGCCTAIKCYGATGCYGGGAGGCGGTGGTTACACAYITC
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1 (bases 1 to 977)
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FEBS Lett. 487 (1), 66-70 (2000)
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/db_xref="taxon:28985"
/clone="BAOAB015D09"
/clone_lib="BAOAB"
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/note="similar to Saccharomyces cerevisiae ORF YNL330c
RPD3 ; histone deacetylase B ]*
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Best Local Similarity 61.8%;
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Direct Submission
Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, Pe 5706, 94057 EVPR cedex, FRANCE. (E-mail:
sequefégenoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
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Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
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                                                                                                                                                         CNSO6TTS 907 bp DNA GSS 05-JUL-2001
T3 end of clone AXOAAO01H05 of library AXOAA from strain CBS 7064
of Pichia farinosa, genomic survey sequence.
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the other extremity of this insert.
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2 (bases 1 to 907)
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Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Liorente, B.,
Malpertuy, A., Neuveglise, C., Ozier Kalogeropoulos, O., Potier, S.,
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Geomaic exploration of the hemiascomycetous yeasts: 1. A set of
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/note-"similar to Saccharomyces cerevisiae ORF YGL194c
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de Montigny, J., Spehner, C., Souciet, J., Tekala, F., Dujon, B., Wincker, P., Artiquenave, F. and Polier, S. Genomic exploration of the hemiascomycetous yeasts: 15. Pichia
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/evidence-not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomycetales; Saccharomycetaceae; Pichia.
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Pred. No. 2.6e-53;
2; Mismatches 292;
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/clone-"AX0AA001H05"
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/note-"end : T3"
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AL414998.1 GI:12193655
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Matches 521; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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                   435 attcaatgtcggtgaggattgtcctgtcttcgacggactttttgatttttgccgtgcttc
                                                                                                                                                                                                                                                                                                                    agatattgatgtccaccatggagatggagtggaagaagcgttttacaccactgatagagt
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                                                      880 ATTCAACGTCGGGGATGACTGTCCAGTTTTCGATGGATTGTKTGAATACTGTGGAATTCT
                                                                                                               760 AAACTACGCTGGTGGATTACATCATGCTAAAAAGTCCGAGGCTTCTGGATTTTGTTACTT
                                                                                                                                                                                                                                           aaacgacatcgtgctagggattctggagttgctcaagatgtttaagcgggttctctacat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           855 egatgaaagttteegeagettgtttagacetettateeagaaggttatggaagtgtatea
                                                                                          495 egceggaggitetatiggigetgeegicaaaitaaacagacaggacgetgatategetat
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Blewitt,M., Matz,E.C., Davy,D.F. and Burr,B.
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DEFINITION T3 end of clone AU0AA005D08 of library AU0AA from strain CBS 3082
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/db_xref="taxon:3635"
/clone_lib="six-day Cotton fiber"
/tissue_type="limmature fiber"
/dev_stage="Six days post anthesis"
/lab_host="XLl-Blue"
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                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBluescript II KS+"
161 c 160 g 161 t 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 343.4; DB 1
Pred. No. 1.4e-52;
                                                                                                                                                                                                                   /organism="Gossypium hirsutum
Unpublished (1999)
Contact: Ben Burr
Biology Department
Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
Fax: 516-344-3407
Seq primer: T3 Primer.
Location/Qualifiers
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73.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : Sequencaçope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces extearonyces servazil, Zygosaccharomyces rouxil, Saccharomyces rouxil, Saccharomyces rouxil, Saccharomyces rouxil, and saccharomyces rouxil, contains, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 8 b ware prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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                                                                                                            Saccharomýces kluýveri
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                        Neuveglise, C., Bon, E., Lepingle, A., Wincker, P., Artiguenave, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232 caccogatgaagcctcaccggatccgtatggctcatagcctaatcattcactatcacctc 291
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                                                                                                                                                                                                                             Gaillardin, C. and Casaregola, S. Genomic exploration of the hemiascomycetous yeasts:
Saccharomyces kluyveri, genomic survey sequence.
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/note-"similar to Saccharomyces
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/db_xref="taxon:4934"
/clone="AU0AA005D08"
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                                                                                         Saccharomyces kluyveri
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BF324960 617 bp mRNA EST 21-NOV-2000 su29e12.yl Gm-c1068 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1068-624 5' similar to TR:Q9ZTP8 Q9ZTP8 HISTONE DEACETYLASE.;
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                          803 CAPACTGATGAATACATTGACTTTTTATCACGTGTTACCCCAGATAACTTGAACATGTTC 744
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                                                                                                                       412 teogetycacgaaacetaaggegatteaatyteggtyaygattyteetytettegaegga
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1045 gtgttgggttgatgaagggtatactattcgaaatgttgcccgttgctggtgttatgagact 1104

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Another—Western: pBluescript II SK+; Site_I: EcoRI; Site_2:
XhoI: The CDNA library was constructed from mRNA isolated
from drought stressed leaf tissue of the cultivar Williams
82. The month old greenhouse grown plants were deprived of
water for 3 days prior to harvesting the stressed leaf
tissue. Complementary DNA was synthesized from mRNA using
a primer consisting of a poly(dT) sequence with a XhoI
restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The
EcoRI-XhoI restriction site of the pBluescript vector. The
ligated CDNA fragments were transformed into DH10B host
cells (GibcoBRL). This library was constructed in the
laboratory of Dr. Randy Shoemaker. I others
                 Shoemaker, R., Kein, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Email: estëwatson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 6313 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
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                                                                                                                                                                                                                                                                                                                                                63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.9%; Score 341; DB 11; Length 6; 74.6%; Pred. No. 3.7e-52; tive 0; Mismatches 146; Indels
                                                                                                                                                                                                                      Unpublished (1999) Contact: Shoemaker K/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine Washington Park Parkway, Box 8501, St. Louis, MO Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Glycine max"
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/lab_host="DH10B"
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Anote—"Organ: Drain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 919)
1 (bases 1 to 919)
1 Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDMA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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                                                                                                                                                                                                                                             AL531607 919 bp mRNA EST 13-FEB-2001 AL531607 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DM002YH15
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                      1165 ttoggcccagattatacgcttcatgtcgacccaagtcctatggagaatttaaacacgccc
                                                         gcagttgctgttggagtagagccggacaacaactcccttacaatgagtatttgagtat
                                                                                              363 GCAGTGGCAGTAGGAGTGGAGCCTAGTCCTAAGTTGCCTTACAATGAATAT
423 TTTGGCCCGGACTATAATCTTCATGTTGAGCCATCCACAATGGAAAACCTAAACACCC
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/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="LTI_NFL001_NBC4"
/sex="male"
                                                                                                                                                                                                                                                                                                       1285 cctagcgtccagtttcagcacaccaccagtca 1318
                                                                                                                                                                                                                                                                                                                            543 CGCAGTGCACCTTTTCAAACAACACCATCGGTCA 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODM002YH15"
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van der Hoeven,R.S., Bezzerides,J.L., Matern,A.L., Holt,J.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Glovannoni,J.J. and Tanksley,S.D. Generation of ESTs from tomato flower tissue
Contact: CUGI
                                                                                                                                                                                                                                                                                                 /clone_lib="tomato flower buds 3.8 mm, Cornell University"
/tissue_type="flower"
/tissue_type="flower"
/tissue_type="flower"
/dev_stage="3.8mm buds"
/note="Wector: pBlueScript SK(-): Site_1: EcoRI: Site_2:
Xhol; supplier: Tanksley: Flower buds and flowers were
taken from greenhouse plants (4.8 wks old, TA495). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 TIGCTICAACTIGICIGICAAGGGCCAIGCCGCTIGCCIIAGGIACCTCAGAICCTICAA 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      792 agatgitggcgctgaaaaagggaaatactatgctctaaatgttccactaaacgatggtat 851
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                                                                                                                                         100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
                                                                                                                                                                                                                               /organism="Lycopersicon esculentum"
/cultivar="mp496"
/db_xref="taxon:4081"
/clone="cTO86011"
                                                                                                        Clemson University Genomics Institute
Clemson University
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/ Organism="Arabidopsis thaliana"
/ Strain="var columbia"
/ db_xref="taxon:3702"
/ clone="164A11XP"

                                                                AA394745 431 bp mRNA EST 30-OCT-1997
26542 Lambda-PRL2 Arabidopsis thaliana cDNA clone 164A11XP 3', mRNA
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Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel E. and Somerville, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MSU-DOE Plant Research Laboratory Michigan State University
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Seq primer: M13 -21 dye primer.
Locatlon/Qualifiers
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AA394745.1 GI;2047956
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Fax: 517-353-9168
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 847)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                         1664 attgattagaacagtgacaactgactagtattttggcccaagttagaaaatcagaatatg 1723
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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354 ttcgccggagtatgttgacttcctcgcttccgtttcgccggaatctatgggcgatccttc 413
     acaggacgetgatategetateaattggggeggtgggetteaecatgetaagaaaagega 593
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